

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.  
 Lal, Preeti  
 Tang, Y. Tom  
 Yue, Henry  
 Corley, Neil C.

(ii) TITLE OF THE INVENTION: KINESIN LIGHT CHAIN HOMOLOG

(iii) NUMBER OF SEQUENCES: 3

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 (B) STREET: 3174 Porter Dr.  
 (C) CITY: Palo Alto  
 (D) STATE: CA  
 (E) COUNTRY: USA  
 (F) ZIP: 94304

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
 (B) COMPUTER: IBM Compatible  
 (C) OPERATING SYSTEM: DOS  
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
 (B) FILING DATE: Filed Herewith

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:  
 (B) FILING DATE:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.  
 (B) REGISTRATION NUMBER: 36,749  
 (C) REFERENCE/DOCKET NUMBER: PF-0484 US

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555  
 (B) TELEFAX: 650-845-4166

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 619 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: SMCANOT01  
 (B) CLONE: 2479739

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ser	Gly	Leu	Val	Leu	Gly	Gln	Arg	Asp	Glu	Pro	Ala	Gly	His	Arg
1				5				10						15	
Leu	Ser	Gln	Glu	Glu	Ile	Leu	Gly	Ser	Thr	Arg	Leu	Val	Ser	Gln	Gly
			20					25					30		
Leu	Glu	Ala	Leu	Arg	Ser	Glu	His	Gln	Ala	Val	Leu	Gln	Ser	Leu	Ser
			35				40					45			
Gln	Thr	Ile	Glu	Cys	Leu	Gln	Gln	Gly	Gly	His	Glu	Glu	Gly	Leu	Val
50						55					60				

0506614 00049  
 0506614 00049

His Glu Lys Ala Arg Gln Leu Arg Arg Ser Met Glu Asn Ile Glu Leu  
 65 70 75 80  
 Gly Leu Ser Glu Ala Gln Val Met Leu Ala Leu Ala Ser His Leu Ser  
 85 90 95  
 Thr Val Glu Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu  
 100 105 110  
 Cys Gln Glu Asn Gln Trp Leu Arg Asp Glu Leu Ala Gly Thr Gln Gln  
 115 120 125  
 Arg Leu Gln Arg Ser Glu Gln Ala Val Ala Gln Leu Glu Glu Glu Lys  
 130 135 140  
 Lys His Leu Glu Phe Leu Gly Gln Leu Arg Gln Tyr Asp Glu Asp Gly  
 145 150 155 160  
 His Thr Ser Glu Glu Lys Glu Gly Asp Ala Thr Lys Asp Ser Leu Asp  
 165 170 175  
 Asp Leu Phe Pro Asn Glu Glu Glu Glu Asp Pro Ser Asn Gly Leu Ser  
 180 185 190  
 Arg Gly Gln Gly Ala Thr Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro  
 195 200 205  
 Ala Arg Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ala Gln  
 210 215 220  
 Gly Arg Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp  
 225 230 235 240  
 Leu Glu Arg Thr Ser Gly Arg Gly His Pro Asp Val Ala Thr Met Leu  
 245 250 255  
 Asn Ile Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Glu Ala  
 260 265 270  
 Ala His Leu Leu Asn Asp Ala Leu Ser Ile Arg Glu Ser Thr Leu Gly  
 275 280 285  
 Pro Asp His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu  
 290 295 300  
 Tyr Gly Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Gln Arg  
 305 310 315 320  
 Ala Leu Glu Ile Arg Glu Lys Val Leu Gly Thr Asn His Pro Asp Val  
 325 330 335  
 Ala Lys Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys  
 340 345 350  
 Tyr Glu Ala Val Glu Arg Tyr Tyr Gln Arg Ala Leu Ala Ile Tyr Glu  
 355 360 365  
 Gly Gln Leu Gly Pro Asp Asn Pro Asn Val Ala Arg Thr Lys Asn Asn  
 370 375 380  
 Leu Ala Ser Cys Tyr Leu Lys Gln Gly Lys Tyr Ala Glu Ala Glu Thr  
 385 390 395 400  
 Leu Tyr Lys Glu Ile Leu Thr Arg Ala His Val Gln Glu Phe Gly Ser  
 405 410 415  
 Val Asp Asp Asp His Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu  
 420 425 430  
 Glu Met Ser Lys Ser Arg His His Glu Gly Gly Thr Pro Tyr Ala Glu  
 435 440 445  
 Tyr Gly Gly Trp Tyr Lys Ala Cys Lys Val Ser Ser Pro Thr Val Asn  
 450 455 460  
 Thr Thr Leu Arg Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Leu  
 465 470 475 480  
 Glu Ala Ala Glu Thr Leu Glu Glu Cys Ala Leu Arg Ser Arg Arg Gln  
 485 490 495  
 Gly Thr Asp Pro Ile Ser Gln Thr Lys Val Ala Glu Leu Leu Gly Glu  
 500 505 510  
 Ser Asp Gly Arg Arg Thr Ser Gln Glu Gly Pro Gly Asp Ser Val Lys  
 515 520 525  
 Phe Glu Gly Gly Glu Asp Ala Ser Val Ala Val Glu Trp Ser Gly Asp  
 530 535 540  
 Gly Ser Gly Thr Leu Gln Arg Ser Gly Ser Leu Gly Lys Ile Arg Asp  
 545 550 555 560  
 Val Leu Arg Arg Ser Ser Glu Leu Leu Val Arg Lys Leu Gln Gly Thr  
 565 570 575  
 Glu Pro Arg Pro Ser Ser Ser Asn Met Lys Arg Ala Ala Ser Leu Asn  
 580 585 590  
 Tyr Leu Asn Gln Pro Ser Ala Ala Pro Leu Gln Val Ser Arg Gly Leu

595 600 605  
 Ser Ala Ser Thr Met Asp Leu Ser Ser Ser Ser  
 610 615

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2453 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SMCANOT01  
 (B) CLONE: 2479739

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGAAGTGGT GAAAGAAGGG GTGGGAACGC TGGACTTCTG GACTTTGGGC AGGGCAGATC 60  
 CTCTGACTCT CTGGCTGCAG AACAGTTTCT TCCGTGCTCT GGCCTGAGTG CCCACAGGCC 120  
 AGGGGCCTCT GCTCTGTACA CAGACCGGGC AAGGTCCCCC AGGCCAGGAT GTCAGGCCTG 180  
 GTGTTGGGGC AGCGGGATGA GCCTGCAGGC CACCGGCTCA GCCAAGAGGA GATCCTGGGG 240  
 AGCACACGGC TGGTCAGCCA AGGGCTAGAG GCCCTACGCA GTGAACACCA GGCCGTGCTG 300  
 CAAAGCCTGT CCCAGACCAT TGAGTGTCTG CAGCAGGGAG GCCATGAGGA AGGGCTGGTG 360  
 CATGAGAAGG CCCGGCAGCT TCGCCGTTCT ATGGAACAACA TTGAGCTCGG GCTGAGTGAG 420  
 GCCCAGGTGA TGCTGGCTCT AGCCAGCCAC CTGAGCACAG TGGAGTCGGA GAAACAGAAG 480  
 CTGCGGGCTC AGGTGCGGCG GCTATGCCAG GAGAACCAGT GGCTGCGGGA TGAGCTGGCT 540  
 GGCACCCAGC AGCGGCTACA GCGCAGTGAA CAGGCTGTGG CTCAGCTGGA GGAGGAAAAG 600  
 AAGCACCTGG AGTTCCTGGG GCAGCTGCGG CAGTATGATG AGGATGGACA TACCTCGGAG 660  
 GAGAAAGAAG GCGATGCCAC CAAGGATTCC CTGGATGACC TCTTTCCTAA TGAGGAGGAA 720  
 GAGGACCCCA GCAATGGCTT GTCCCGTGGT CAAGGTGCTA CAGCAGCTCA GCAGGGTGGA 780  
 TATGAGATCC CAGCAAGGTT GCGGACGTTG CACAACCTGG TGATCCAGTA CGCAGCCCAA 840  
 GGTGCGTATG AGGTGGCCGT GCCACTCTGT AAGCAGGCAC TAGAGGACCT GGAGGAAAAG 900  
 TCAGGCCGTG GCCACCCTGA TGTCGCCACC ATGCTCAACA TCCTTGCTTT GGTGTATCGT 960  
 GACCAGAATA AGTATAAGGA AGCTGCCCAC CTGCTGAATG ATGCCCTTAG CATCCGGGAG 1020  
 AGCACCTTGG GACCTGACCA TCCTGCTGTG GCTGCCACAC TCAACAATTT GGCTGTGCTC 1080  
 TATGGCAAAA GGGGCAAGTA CAAGGAGGCA GAGCCTCTGT GCCAGCGGGC ACTGGAGATT 1140  
 CGAGAAAAGG TCCTGGGCAC GAATCATCCA GATGTGGCAA AACAGCTGAA CAACCTGGCC 1200  
 CTCTTGTGCC AAAACCAGGG CAAGTATGAG GCCGTGGAAC GCTACTACCA GCGAGCACTG 1260  
 GCCATCTACG AGGGGCAGCT GGGGCCGGAC AACCCTAATG TAGCCCGGAC CAAGAACAAC 1320  
 CTGGCTTCCT GTTACCTGAA ACAGGGCAAA TATGCTGAGG CTGAGACACT ATACAAAGAG 1380  
 ATCCTGACCC GTGCCCATGT ACAGGAGTTT GGGTCTGTGG ATGATGACCA CAAGCCCATC 1440  
 TGGATGCATG CAGAGGAGCG CAGAGAAATG AGCAAAAGCC GGCACCATGA GGGTGGGACA 1500  
 CCCTATGCTG AGTATGGAGG CTGGTACAAG GCCTGCAAAG TGAGCAGCCC CACAGTGAAC 1560  
 ACTACTCTGA GAAACCTGGG AGCTCTGTAT AGGCGCCAGG GAAAGCTGGA GGCTGCTGAG 1620  
 ACCCTGGAGG AATGTGCCCT GCGGTCCCAG AGACAGGGCA CTGACCCTAT CAGCCAGACG 1680  
 AAGGTGGCAG AGCTGCTTGG GGAGAGTGAT GGTAGAAGGA CCTCCCAGGA GGGCCCTGGA 1740  
 GACAGTGTGA AATTCGAGGG TGGTGAAGAT GCTTCTGTGG CTGTGGAGTG GTCCGGGGAT 1800  
 GGCAGTGGGA CCCTGCAGAG GAGTGGCTCT CTTGGCAAGA TCCGGGATGT GCTCCGCAGA 1860  
 AGCAGTGAAC TCTTGGTGAG GAAGCTCCAG GGGACTGAGC CTCGGCCCTC CAGCAGCAAC 1920  
 ATGAAGCGAG CAGCCTCCTT GAACTATCTG AACCAACCTA GTGCAGCACC CCTCCAGGTC 1980  
 TCCCGGGGCC TCAGTGCCAG CACCATGGAC CTCTCTTCAA GCAGCTGACA TTCAACCCGG 2040  
 CCCCCAGGTC TGCTGGGTCC CCCCACCCCC ACAGCCCTCA CAGCATTCCC CATTGCTCCT 2100  
 GGCTCTTCCC CACCCCTAGG TGGGACAGTG AAGGGGAGCA GTTAAACCAG AAGATTGCTG 2160  
 CTGCCCTTAG GGTCTCAGCT CCCTCCTCAG GAATCCCTCT TAGGAAGGAC CCTCAGGACA 2220  
 CCCTCTCTGC ACCCTGTGGT CCTCTAGAGT AGCTAGCTCT GAGGCCCCAA GGTGGGTACA 2280  
 AAGCAGGTAT GGCCCTCAGA GATGCAGCCT GCTGCTGGCT TTTCAGTCAG AGGGTTGGGG 2340  
 GCTGGCCAGC CAAGCTGCCT TGCCCTGGCC GCTCTTACTC CCTCCCTCTG CTGTCTCACT 2400  
 TCAGGTCCAT GTATTTCACT TTTCTTAAAT AAAAGAATCA GTNCTTNTNT NNG 2453

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 307085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr  
1 5 10 15  
Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu  
20 25 30  
Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Glu Thr  
35 40 45  
Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys  
50 55 60  
Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser  
65 70 75 80  
Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu  
85 90 95  
Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu  
100 105 110  
Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln  
115 120 125  
Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Glu Lys Lys His Leu  
130 135 140  
Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Asp Ile Ser Pro Ser  
145 150 155 160  
Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe  
165 170 175  
Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln Gln His Ser  
180 185 190  
Ser Ala Ala Ala Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro Ala Arg  
195 200 205  
Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ser Gln Gly Arg  
210 215 220  
Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu  
225 230 235 240  
Lys Thr Ser Gly His Asp His Pro Asp Val Ala Thr Met Leu Asn Ile  
245 250 255  
Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Asp Ala Asn  
260 265 270  
Leu Leu Asn Asp Ala Leu Ala Ile Arg Glu Lys Thr Leu Gly Lys Asp  
275 280 285  
His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu Tyr Gly  
290 295 300  
Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Lys Arg Ala Leu  
305 310 315 320  
Glu Ile Arg Glu Lys Val Leu Gly Lys Asp His Pro Asp Val Ala Lys  
325 330 335  
Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys Tyr Glu  
340 345 350  
Glu Val Glu Tyr Tyr Tyr Gln Arg Ala Leu Glu Ile Tyr Gln Thr Lys  
355 360 365  
Leu Gly Pro Asp Asp Pro Asn Val Ala Lys Thr Lys Asn Asn Leu Ala  
370 375 380  
Ser Cys Tyr Leu Lys Gln Gly Lys Phe Lys Gln Ala Glu Thr Leu Tyr  
385 390 395 400  
Lys Glu Ile Leu Thr Arg Ala His Glu Arg Glu Phe Gly Ser Val Asp  
405 410 415  
Asp Glu Asn Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu Glu Cys  
420 425 430  
Lys Gly Lys Gln Lys Asp Gly Thr Ser Phe Gly Glu Tyr Gly Gly Trp  
435 440 445  
Tyr Lys Ala Cys Lys Val Asp Ser Pro Thr Val Thr Thr Thr Leu Lys  
450 455 460  
Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Phe Glu Ala Ala Glu  
465 470 475 480  
Thr Leu Glu Glu Ala Ala Met Arg Ser Arg Lys Gln Gly Leu Asp Asn

**Abstract**